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SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Vinik, Aaron
             Pittenger, Gary
             Rafaeloff, Ronit
             Barlow, Scott

    (ii) TITLE OF THE INVENTION: HIGH LEVEL EXPRESSION OF
         INGAP

    (iii) NUMBER OF SEQUENCES: 6

    (iv) CORRESPONDENCE ADDRESS:
            (A) ADDRESSEE: Banner & Witcoff, Ltd.
            (B) STREET: 1001 G Street, N.W.
            (C) CITY: Washington
            (D) STATE: DC
            (E) COUNTRY: USA
            (F) ZIP: 20001

    (v) COMPUTER READABLE FORM:
            (A) MEDIUM TYPE: Diskette
            (B) COMPUTER: IBM Compatible
            (C) OPERATING SYSTEM: DOS
            (D) SOFTWARE: FastSEQ for Windows Version 2.0

    (vi) CURRENT APPLICATION DATA:
            (A) APPLICATION NUMBER: 08/741,096
            (B) FILING DATE: 30-OCT-1996
            (C) CLASSIFICATION: 435

    (vii) PRIOR APPLICATION DATA:
            (A) APPLICATION NUMBER:
            (B) FILING DATE:

    (viii) ATTORNEY/AGENT INFORMATION:
            (A) NAME: Kagan, Sarah A
            (B) REGISTRATION NUMBER: 32,145
            (C) REFERENCE/DOCKET NUMBER: 0570.01435

    (ix) TELECOMMUNICATION INFORMATION:
            (A) TELEPHONE: 202-508-9100
            (B) TELEFAX: 202-508-9299
            (C) TELEX: 97430 BMB UT

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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 94 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGCAAGACA GGTACCATGA TGCTTCCCAT GACCCTCTGT AGGATGTCTT GGATGCTGCT   60
TTCCTGCCTG ATGTTCCTTT CTTGGGTGGA AGGT   94

    (2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 31 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGCGGATCC CGAAGAATCT CAAAAGAAAC T   31

    (2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 32 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACCGGCTCG AGTGCTCTTC CTGAGTGAAT CC   32

    (2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 558 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
CCGCGGATCC CGAAGAATCT CAAAAGAAAC TGCCTTCTTC ACGTATAACC TGTCCTCAAG    60
GCTCTGTAGC CTATGGGTCC TATTGCTATT CACTGATTTT GATACCACAG ACCTGGTCTA   120
ATGCAGAACT ATCCTGCCAG ATGCATTTCT CAGGACACCT GGCATTTCTT CTCAGTACTG   180
GTGAAATTAC CTTCGTGTCC TCCCTTGTGA AGAACAGTTT GACGGCCTAC CAGTACATCT   240
GGATTGGACT CCATGATCCC TCACATGGTA CACTACCCAA CGGAAGTGGA TGGAAGTGGA   300
GCAGTTCCAA TGTGCTGACC TTCTATAACT GGGAGAGGAA CCCCTCTATT GCTGCTGACC   360
GTGGTTATTG TGCAGTTTTG TCTCAGAAAT CAGGTTTTCA GAAGTGGAGA GATTTTAATT   420
GTGAAAATGA GCTTCCCTAT ATCTGCAAAT TCAAGGTCTA GGGCAGTTCT AATTTCAACA   480
GCTTGAAAAT ATTATGAAGC TCACATGGAC AAGGAAGCAA GTATGAGGAT TCACTCAGGA   540
                                                                   558
AGAGCACTCG AGCCGGTC
```

        (2) INFORMATION FOR SEQ ID NO:5:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 26 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: peptide

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp Met Leu Leu Ser
1               5                   10                  15
Cys Leu Met Phe Leu Ser Trp Val Glu Gly
            20                  25
```

        (2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 175 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp Met Leu Leu Ser
1               5                   10                  15
Cys Leu Met Phe Leu Ser Trp Val Glu Gly Glu Glu Ser Gln Lys Lys
            20                  25                  30
Leu Pro Ser Ser Arg Ile Thr Cys Pro Gln Gly Ser Val Ala Tyr Gly
        35                  40                  45
Ser Tyr Cys Tyr Ser Leu Ile Leu Ile Pro Gln Thr Trp Ser Asn Ala
    50                  55                  60
Glu Leu Ser Cys Gln Met His Phe Ser Gly His Leu Ala Phe Leu Leu
```

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```
65                          70                       75                      80
Ser Thr Gly Glu Ile Thr Phe Val Ser Ser Leu Val Lys Asn Ser Leu
                    85                       90                      95
Thr Ala Tyr Gln Tyr Ile Trp Ile Gly Leu His Asp Pro Ser His Gly
            100                     105                     110
Thr Leu Pro Asn Gly Ser Gly Trp Lys Trp Ser Ser Ser Asn Val Leu
            115                     120                     125
Thr Phe Tyr Asn Trp Glu Arg Asn Pro Ser Ile Ala Ala Asp Arg Gly
        130                     135                     140
Tyr Cys Ala Val Leu Ser Gln Lys Ser Gly Phe Gln Lys Trp Arg Asp
145                     150                     155                     160
Phe Asn Cys Glu Asn Glu Leu Pro Tyr Ile Cys Lys Phe Lys Val
                165                     170                     175
```